

Appendix IV

Alignment of instant SEQ ID NO: 3 with GenBank Accession No. K00470

```
>| K00470.1|HUMAN| Homo sapiens growth hormone variant precursor (GH-V) gene, complete  
cds  
Length=2660  
  
GENE_ID: 2883 GENE: growth hormone 2 [Homo sapiens] (Over 10 PubMed links)  
  
Score = 4913 bits (2660), Expect = 0.0  
Identities = 2660/2660 (100%), Gaps = 0/2660 (0%)  
Strand=Plus/Plus  
  
Query 1      GAATTCACTGAAATCATGCCAGAACCCCGCAATCTTATGGCTGTGCCTTTGGCCCT 60  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 1      GAATTCACTGAAATCATGCCAGAACCCCGCAATCTTATGGCTGTGCCTTTGGCCCT 60  
  
Query 61     TTTCCCACACACACATTCTGTCTGGTGGGGAGGGGAAACATGCCGGGAGGAGAAG 120  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 61     TTTCCCACACACACATTCTGTCTGGTGGGGAGGGGAAACATGCCGGGAGGAGAAG 120  
  
Query 121    GAATAGGATAGAGAGTGGGATGGGTGGTAGGGTCTCAAGGACTGGCTATCCTGACA 180  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 121    GAATAGGATAGAGAGTGGGATGGGTGGTAGGGTCTCAAGGACTGGCTATCCTGACA 180  
  
Query 181     TCCTTCCTCCGGTTCAGGGTGGCCACCCTGGGCTGCTGCCAG&GGGACCC 240  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 181     TCCTTCCTCCGGTTCAGGGTGGCCACCCTGGGCTGCTGCCAG&GGGACCC 240  
  
Query 241     TTAAAGAGAGGACAAAGTTGGGTGTATCTCTGGACATTTCTGTGACAAACCCCTCACAA 300  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 241     TTAAAGAGAGGACAAAGTTGGGTGTATCTCTGGACATTTCTGTGACAAACCCCTCACAA 300  
  
Query 301     CGCTGGTGATGGTGGGAAGGGAAAGATGACAAAGTCAGGGGGCATGATCCCAGCATGTGTG 360  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 301     CGCTGGTGATGGTGGGAAGGGAAAGATGACAAAGTCAGGGGGCATGATCCCAGCATGTGTG 360  
  
Query 361     GGAGGGAGCTTCTRAATTATTCATTAGCACA&GCCCGTCAGTGGCCCCAGGCCCTAAACATG 420  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 361     GGAGGGAGCTTCTRAATTATTCATTAGCACA&GCCCGTCAGTGGCCCCAGGCCCTAAACATG 420  
  
Query 421     CAGAGAAAACAGGTGAGGGAGAACGAGCAGAGAGAGAAGGGGCCAGGTATAAAAGGGCCAC 480  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 421     CAGAGAAAACAGGTGAGGGAGAACGAGCAGAGAGAGAAGGGGCCAGGTATAAAAGGGCCAC 480  
  
Query 481     AAGAGACCAGCTCAGGGATCCAAAGGCCAAACTCCCCGAACCACTCAGGGTCTGTGGAC 540  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 481     AAGAGACCAGCTCAGGGATCCAAAGGCCAAACTCCCCGAACCACTCAGGGTCTGTGGAC 540  
  
Query 541     AGCTCACTAGCGGCA&TGGCTGCAGGTAAAGC GCCCTAA&ATCCCCTTIGGCACAATGTGT 600  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 541     AGCTCACTAGCGGCAATGGCTGCAGGTAAAGC GCCCTAA&ATCCCCTTIGGCACAATGTGT 600  
  
Query 601     CCTGAGGGGAGAGGGCGGCCCTCTGTAGATGGCACGGGGCACTAAACCCCTCAGGTTTGGGG 660  
|||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 601     CCTGAGGGGAGAGGGCGGCCCTCTGTAGATGGCACGGGGCACTAAACCCCTCAGGTTTGGGG 660  
  
Query 661     CTTATGAATGTTAGCTATCGCCATCTAAGGCCAGTATTTGGCAATCTCTGAATGTTCT 720  
|||||||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 661     CTTATGAATGTTAGCTATCGCCATCTAAGGCCAGTATTTGGCAATCTCTGAATGTTCT 720  
  
Query 721     GGTCCCCTGGAGGGAGGGCAGAGAGAGAGAGAGGAAAAAAACCC&GCTCCTGGAACAGG 780  
|||||||||||||||||||||||||||||||||||||||||||||||  
Sbjct 721     GGTCCCCTGGAGGGAGGGCAGAGAGAGAGAGG&GAGAG&GAGAG&GAGAG&GAGAG 780  
  
Query 781     GAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTGCCCTCCGGTTCTCCCCAGGCTC 840  
|||||||||||||||||||||||||||||||||||||||||||  
Sbjct 781     GAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTGCCCTCCGGTTCTCCCCAGGCTC 840
```

Query	841	CCGGACGTCCCTGCTCCTGGCTTTGGCCTGCTCTGCCTGTCTGGCTCAAGAGGGCAG	900
Sbjct	841	CCGGACGTCCCTGCTCCTGGCTTTGGCCTGCTCTGCCTGTCTGGCTCAAGAGGGCAG	900
Query	901	TGCCCTCCCAACCATTCCCTTATCCAGGGTTTTTGACAACGCTATGCCCGCGCCCCGTG	960
Sbjct	901	TGCCCTCCCAACCATTCCCTTATCCAGGGTTTTTGACAACGCTATGCCCGCGCCCCGTG	960
Query	961	CCTGTACCAAGCTGGCATATGACACCTATCAGGAGTTGTAAAGCTCTGGGTAAATGGGTGC	1020
Sbjct	961	CCTGTACCAAGCTGGCATATGACACCTATCAGGAGTTGTAAAGCTCTGGGTAAATGGGTGC	1020
Query	1021	GCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCTCCCCTGGGAAGTAATGGGAGGAGACTA	1080
Sbjct	1021	GCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCTCCCCTGGGAAGTAATGGGAGGAGACTA	1080
Query	1081	AGGAGCTCAGGGTTGTTCTGAAGTGAATAATGCAGGGCAGATGACCATACGCTGAGTGAG	1140
Sbjct	1081	AGGAGCTCAGGGTTGTTCTGAAGTGAATAATGCAGGGCAGATGACCATACGCTGAGTGAG	1140
Query	1141	GTTCCCAGAAAAGTAACAAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGCGGTCTT	1200
Sbjct	1141	GTTCCCAGAAAAGTAACAAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGCGGTCTT	1200
Query	1201	CTCTCTAGGAAGAACGCCTATATCCTGAAGGAGCAGAACTATTCAATTCTGCAGAACCCCCA	1260
Sbjct	1201	CTCTCTAGGAAGAACGCCTATATCCTGAAGGAGCAGAACTATTCAATTCTGCAGAACCCCCA	1260
Query	1261	GACCTCCCTCTGCTTCTCAGAGTCTATTCAAACACCTTCAACAGGGTGAAAACGCAGCA	1320
Sbjct	1261	GACCTCCCTCTGCTTCTCAGAGTCTATTCAAACACCTTCAACAGGGTGAAAACGCAGCA	1320
Query	1321	GAATCTGTGAGTGGATGCCTTCTCCCCAGGTGGATGGGTAGACCTGTGGTAGAGGCC	1380
Sbjct	1321	GAATCTGTGAGTGGATGCCTTCTCCCCAGGTGGATGGGTAGACCTGTGGTAGAGGCC	1380
Query	1381	CCCCGGCAGCACAGCCACTGCCCGTCTTCCCTGCAAGAACCTAGAGCTGCTCCGCATCT	1440
Sbjct	1381	CCCCGGCAGCACAGCCACTGCCCGTCTTCCCTGCAAGAACCTAGAGCTGCTCCGCATCT	1440
Query	1441	CCCTGCTGCTCATCCAGTCATGGCTGGAGCCCTGCAAGCTCCTCAGGGAGGTCTTCCCA	1500
Sbjct	1441	CCCTGCTGCTCATCCAGTCATGGCTGGAGCCCTGCAAGCTCCTCAGGGAGGTCTTCCCA	1500
Query	1501	ACAGCCCTGGGTATGGCGCCTCGGACAGCAACGTCTATGCCACCTGAAGGACCTAGAGG	1560
Sbjct	1501	ACAGCCCTGGGTATGGCGCCTCGGACAGCAACGTCTATGCCACCTGAAGGACCTAGAGG	1560
Query	1561	AAGGCATCCAACCGCTGATGTGGGTGAGGGTGGCACCCAGGATCCAATCTGGGGCCCCAC	1620
Sbjct	1561	AAGGCATCCAACCGCTGATGTGGGTGAGGGTGGCACCCAGGATCCAATCTGGGGCCCCAC	1620
Query	1621	TGGCTTCCAGGGACTGGGGAGAGAAAACACTGCTGCCCTCTTTTAGCAGTCAGGCCTGA	1680
Sbjct	1621	TGGCTTCCAGGGACTGGGGAGAGAAAACACTGCTGCCCTCTTTTAGCAGTCAGGCCTGA	1680
Query	1681	CCCAAGAGAACTCACCGTATTCTCTCATTCCTCCCTGCTGAATCCTCCAGGCCCTCTCTAC	1740
Sbjct	1681	CCCAAGAGAACTCACCGTATTCTCTCATTCCTCCCTGCTGAATCCTCCAGGCCCTCTCTAC	1740
Query	1741	AACCTGGAGGGAGGGAGGAATAATGGATGAATGAGAGAGGGAGGGAAACAGTGCCTAACGCG	1800
Sbjct	1741	AACCTGGAGGGAGGGAGGAATAATGGATGAATGAGAGAGGGAGGGAAACAGTGCCTAACGCG	1800
Query	1801	CTTGGCCTCTCCCTCTCTTCCCTCACTTTCAGGAGGTGGA>GGCAGCCCCCGGACT	1860
Sbjct	1801	CTTGGCCTCTCCCTCTCTTCCCTCACTTTCAGGAGGTGGA>GGCAGCCCCCGGACT	1860
Query	1861	GGGCAGATCTCAATCAGTCCTACAGCAAGTTGACACAAATGCCAACGATGACGCCA	1920
Sbjct	1861	GGGCAGATCTCAATCAGTCCTACAGCAAGTTGACACAAATGCCAACGATGACGCCA	1920
Query	1921	CTGCTCAAGAACTACGGGCTGCTACTGCTTCAGGAAGGGACATGGACAAAGGTGAGACA	1980
Sbjct	1921	CTGCTCAAGAACTACGGGCTGCTACTGCTTCAGGAAGGGACATGGACAAAGGTGAGACA	1980
Query	1981	TTCTGCGCATCGTGCAGTGCCTCGTCTGCTGGAGGGCAGCTGTGGCTTAGCTGCCCGGG	2040
Sbjct	1981	TTCTGCGCATCGTGCAGTGCCTCGTCTGCTGGAGGGCAGCTGTGGCTTAGCTGCCCGGG	2040

Query	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCCCTCTGGTGGAAAGGTGCTACTCCAGTG 	2100
Sbjct	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCCCTCTGGTGGAAAGGTGCTACTCCAGTG 	2100
Query	2101	CCCACCAGCCTGTCTTAATAAAATTAA>GTGATCATTTTGTTGACTTAGGTGTCTTG 	2160
Sbjct	2101	CCCACCAGCCTGTCTTAATAAAATTAA>GTGATCATTTTGTTGACTTAGGTGTCTTG 	2160
Query	2161	TATAATATTATGGGTGGAGGCCGGTGGTATGGAGCAAGGGGCCAGGTGGGAAGACAAAC 	2220
Sbjct	2161	TATAATATTATGGGTGGAGGCCGGTGGTATGGAGCAAGGGGCCAGGTGGGAAGACAAAC 	2220
Query	2221	CTGTAGGGCCTTCAGGGTCTATTCGGGA&CCAGGCTGGAGTGCACTGGCAGTCTGGCTC 	2280
Sbjct	2221	CTGTAGGGCCTTCAGGGTCTATTCGGGA&CCAGGCTGGAGTGCACTGGCAGTCTGGCTC 	2280
Query	2281	GCTGCAATCTCCGCCTCTGGGTCAAGCGATTCTCGCCTCAGTCCTCCGAATAGTTG 	2340
Sbjct	2281	GCTGCAATCTCCGCCTCTGGGTCAAGCGATTCTCGCCTCAGTCCTCCGAATAGTTG 	2340
Query	2341	CGATTCCAGGCATGCAAGACCAAGGCTCAGCTAATTGGTATTTTGTTGAGACGGGT 	2400
Sbjct	2341	CGATTCCAGGCATGCAAGACCAAGGCTCAGCTAATTGGTATTTTGTTGAGACGGGT 	2400
Query	2401	TTCACCATATTGGCCAGTCTGGTCTCCATCTGACCTCAGGTAAATCCGCCGCCCTCGG 	2460
Sbjct	2401	TTCACCATATTGGCCAGTCTGGTCTCCATCTGACCTCAGGTAAATCCGCCGCCCTCGG 	2460
Query	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCTGTGATT 	2520
Sbjct	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCTGTGATT 	2520
Query	2521	TAATAATAATTATACCAAGCAGAACGACGTCACACACAGCATGGCTACCTGGCCATGCC 	2580
Sbjct	2521	TAATAATAATTATACCAAGCAGAACGACGTCACACACAGCATGGCTACCTGGCCATGCC 	2580
Query	2581	AGCC>GG&ATTG>GTGTTGCTTGGCACTGTCTCTCATGCAATTGGGTCCACTC 	2640
Sbjct	2581	AGCCAGTGGACATTGAGTGTGTTGCTTGGCACTGTCTCTCATGCAATTGGGTCCACTC 	2640
Query	2641	AGTAGATGCTTGTGAATTTC 2660 	
Sbjct	2641	AGTAGATGCTTGTGAATTTC 2660 	